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## Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the

application:

## Listing of Claims:

Claims 1-25 (cancelled)

26. (original) A method for determining whether a transcript is present in a biological

sample comprising:

      providing a plurality of perfect match intensity values ($PM_i$) and

background intensity values ($B_i$) for said transcript, wherein each of said $PM_i$ is

paired with one of said $B_i$;

      calculating a $p$ value using one sided Wilcoxon's signed rank test, wherein

said $p$ value is for a null hypothesis that $\theta =$ a threshold value and an alternative

hypothesis that said $\theta >$ said threshold value, wherein said $\theta$ is a test statistic for

intensity difference between said perfect match intensity values and background

intensity values; and

      indicating whether said transcript is present based upon said $p$ value.


27. (Original) The method of Claim 26 wherein said testing statistic is $median(PM_i\text{-}B_i)$.


28. (Original) The method of Claim 27 wherein said threshold value is zero.

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29. (Previously presented) The method of Claim 27 wherein said threshold value is

calculated using:   $\tau_3 = c_3 \sqrt{\overline{median(PM_i)}}$  wherein said $c_3$ is a constant.

30. (Original) The method of Claim 27 wherein threshold value is calculated

using:   $\tau_3 = c_3 \sqrt{\overline{mean(PM_i)}}$  wherein said $c_3$ is a constant.

31. (Original) The method of Claim 27 wherein said step of indicating comprises

indicating said transcript is present if said $p$ is smaller than a first significance level ($\alpha_1$).

32. (Original) The method of Claim 31 wherein said significance level is 0.01-0.08.

33. (Original) The method of Claim 32 wherein said first significance level is 0.04.

34. (Original) The method of Claim 31 wherein said step of indicating further comprises

indicating said transcript is absent if said $p$ is greater than a second significance level

($\alpha_2$).

35. (Canceled)

36. (Previously presented) The method of Claim 34 wherein said second significance

level is 0.06.

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37. (Previously presented) The method of Claim 34 wherein said first significance level

($\alpha_1$) is smaller than said ($\alpha_2$) and said step of indicating further comprises indicating said

transcript is marginally detected if $\alpha_1 \leq p < \alpha_2$.

38. (Original) The method of Claim 37 where first significance level is 0.04 and second

significance level is 0.06.

Claims 39-63 (cancelled)

64. (Previously presented) A computer software product comprising:

computer program code for providing a plurality of perfect match intensity

values ($PM_i$) and background intensity values ($B_i$) for a transcript, wherein each of

said $PM_i$ is paired with one of said $B_i$;

computer program code for calculating a $p$ value using one sided

Wilcoxon's signed rank test, wherein said $p$-value is for a null hypothesis that

$\theta$=a threshold value and an alternative hypothesis that said $\theta$> said threshold

value, wherein said $\theta$ is a test statistic for intensity difference between said perfect

match intensity values and background intensity values; and

computer program code for indicating whether said transcript is present

based upon said $p$-value; and

a computer readable medium that stores said codes.

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65. (Original) The computer software product of Claim 64 wherein said testing statistic is $median(PM_i\text{-}B_i)$.

66. (Original) The computer software product of Claim 65 wherein said threshold value is zero.

67. (Previously presented) The computer software product of Claim 66 wherein said threshold value is calculated using:   $\tau_3 = c_3\sqrt{median(PM_i)}$   wherein said $c_3$ is a constant.

68. (Original) The computer software product of Claim 66 wherein threshold value is calculated using:   $\tau_3 = c_3\sqrt{mean(PM_i)}$   wherein said $c_3$ is a constant.

69. (Original) The computer software product of Claim 66 wherein said step of indicating comprises indicating said transcript is present if said $p$ is smaller than a first significance level ($\alpha_1$).

70. (Original) The computer software product of Claim 69 wherein said significance level is 0.01-0.08.

71. (Original) The computer software product of Claim 70 wherein said first significance level is 0.04.

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72. (Original) The computer software product of Claim 71 wherein said computer software code of indicating further comprises computer software code for indicating that said transcript is absent if said $p$ is greater than or equal to a second significance level ($\alpha_2$).

73. (Canceled)

74. (Previously presented) The computer software product of Claim 72 wherein said second significance level is 0.06.

75. (Previously presented) The computer software product of Claim 72 wherein said first significance level ($\alpha_1$) is smaller than said ($\alpha_2$) and said code for indicating further comprises code for indicating that said transcript is marginally detected if $\alpha_1 \leq p < \alpha_2$.

76. (Original) The computer software product of Claim 75 where first significance level is 0.04 and second significance level is 0.06.

Claims 77-89 (cancelled)

90. ( Previously presented) The computer software product of Claim 76 wherein said testing statistic is $median((PM_i\text{-}MM_i)/(PM_i + MM_i))$.

Claims 91-101 (cancelled)

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102. (Previously presented) A system for determining whether a transcript is present in a biological sample comprising:

a processor; and

a memory being coupled to the processor, the memory storing a plurality of machine instructions that cause the processor to perform a plurality of logical steps when implemented by the processor; said logical steps comprising:

providing a plurality of perfect match intensity values ($PM_i$) and background intensity values ($B_i$) for said transcript, wherein each of said $PM_i$ is paired with one of said $B_i$;

calculating a $p$ value using one sided Wilcoxon's signed rank test, wherein said $p$ value is for a null hypothesis that $\theta$=a threshold value and an alternative hypothesis that said $\theta >$ said threshold value, wherein said $\theta$ is a test statistic for intensity difference between said perfect match intensity values and background intensity values; and

indicating whether said transcript is present based upon said $p$ value.


103. (Previously presented) A method for determining whether a transcript is present in a biological sample comprising:

providing a plurality of perfect match intensity values ($PM_i$) and mismatch intensity values ($MM_i$) for more than 5000 transcripts, wherein the $PM_i$ for each of said 5000 transcripts is paired with one of the $MM_i$;

calculating a $p$-value using one-sided Wilcoxon's signed rank test, wherein the $p$-value is for a null hypothesis that $\theta$=a threshold value and an

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alternative hypothesis that said $\theta>$ said threshold value, wherein said $\theta$ is a test

statistic for intensity difference between said perfect match intensity values and

mismatch intensity values; and

indicating whether said transcript is present based upon said $p$-value.

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